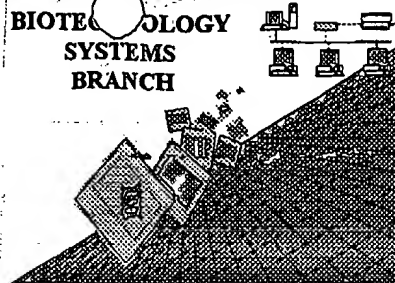


RAW SEQUENCE LISTING ERROR REPORT



0400
91.10.01

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/728,720

Source: OIPE

Date Processed by STIC: 12/28/2000

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THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin30help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

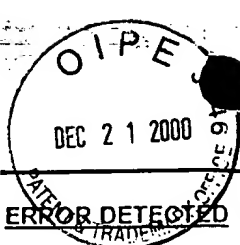
Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>



Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER:

09/728,720

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 ☐ Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 ☐ Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 ☐ Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 ☐ Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 ☐ Variable Length Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 ☐ PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 8 ☐ Skipped Sequences (OLD RULES) Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS: (Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 ☐ Skipped Sequences (NEW RULES) Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 10 ☐ Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 ☐ Use of <213>Organism (NEW RULES) Sequence(s) _____ are missing this mandatory field or its response.
- 12 ☐ Use of <220>Feature (NEW RULES) Sequence(s) _____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 ☐ PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

OIPE

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/728,720

DATE: 12/18/2000
 TIME: 14:02:22

Input Set : A:\Stanfor1.app
 Output Set: N:\CRF3\12182000\I728720.raw

Does Not Comply
 Corrected Diskette Needed

MR 4-5

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3 <110> APPLICANT: Pong, Steven K.H.
 4 Hadlock, Kenneth G.
 6 <120> TITLE OF INVENTION: Prevention and Treatment of HCV Infection Employing
 7 Antibodies that Inhibit the Interaction of HCV Virions
 8 with Their Receptor.
 10 <130> FILE REFERENCE: 2002850-0009
 12 <140> CURRENT APPLICATION NUMBER: US/09/728,720
 13 <141> CURRENT FILING DATE: 2000-12-01
 15 <160> NUMBER OF SEQ ID NOS: 35
 17 <170> SOFTWARE: PatentIn Ver. 2.1
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 160
 21 <212> TYPE: DNA
 22 <213> ORGANISM: Hepatitis C Virus
 24 <400> SEQUENCE: 1
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 26 caacaccctg cactgcccga ctgattgctt ccgcaagcat ccggaagcca catactctcg 120
 27 gtgcggctcc ggtccctgga tcaacaccag gtgccttggt 160
 30 <210> SEQ ID NO: 2
 31 <211> LENGTH: 160
 32 <212> TYPE: DNA
 33 <213> ORGANISM: Hepatitis C Virus
 35 <400> SEQUENCE: 2
 36 ctcaactgga ttcaccaaag tgtgcggagc gcccctctgt gtcacgag gggcgggcaa 60
 37 caacaccctg cgtgcccga ctgattgttt ccgcaagcat ccggaagcca cgtactctcg 120
 38 gtgcggctcc ggtccctgga ttaaccccag gtgccttggt 160
 41 <210> SEQ ID NO: 3
 42 <211> LENGTH: 160
 43 <212> TYPE: DNA
 44 <213> ORGANISM: Bovine Pancreatic Ribonuclease A
 46 <400> SEQUENCE: 3
 47 tagtactggg ttcactaaga cgtgcggagg cccccctgt aacacgagg gggcgggtaa 60
 48 ccgacacctg atctgcccga cggactgctt ccggaagcac ccgaggcta cttacacaaa 120
 49 atgtggctcg gggccctggt tgacacctag gtgcctagta 160
 52 <210> SEQ ID NO: 4
 53 <211> LENGTH: 160
 54 <212> TYPE: DNA
 55 <213> ORGANISM: T7 Bacteriophage
 57 <400> SEQUENCE: 4
 58 tggcacaggg ttcaccaaaga cgtgtggggc cccccatgt aacacgagg gggcgggcaa 60
 59 taacaccttg acttgcccga cggactgttt ccggaagcac ccgaggcca cttacacaaa 120
 60 atgtggctcg gggccctggt tgacacctag gtgcctagta 160
 63 <210> SEQ ID NO: 5
 64 <211> LENGTH: 166
 65 <212> TYPE: DNA
 66 <213> ORGANISM: Bacterial Protein
 68 <400> SEQUENCE: 5

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/728,720

DATE: 12/18/2000

TIME: 14:02:22

Input Set : A:\Stanfor1.app

Output Set: N:\CRF3\12182000\I728720.raw

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69 ctccactggc tacaccaaga cttgcggcgc accaccctgc cgcattagag ctgacttcaa 60
70 tgcacagcatg gacttgttgt gccccacgga ctgttttagg aagcatcctg ataccaccta 120
71 catcaaatgt gctctgggc cctggctcac gccaaagtgc ctgatac 166
74 <210> SEQ ID NO: 6
75 <211> LENGTH: 167
76 <212> TYPE: DNA
77 <213> ORGANISM: Artificial Sequence
79 <220> FEATURE:
80 <223> OTHER INFORMATION: Description of Artificial Sequence:Synthetic
82 <400> SEQUENCE: 6
83 ctccactggt tcacaaaac ttgcggcgc ccaccctgcc gcacagagc tgactttaat 60
84 gccagcacgg acctgctgtg cccacggac tgtttcagg agcatcctga agccacttac 120
85 atcaaatgtg gctctgggc cccctgtga gccaaagtgc cctaata 167
88 <210> SEQ ID NO: 7
89 <211> LENGTH: 166
90 <212> TYPE: DNA
91 <213> ORGANISM: Artificial Sequence
93 <220> FEATURE:
94 <223> OTHER INFORMATION: Description of Artificial Sequence:Synthetic
96 <400> SEQUENCE: 7
97 cgggactggg ttcaactaaga catgcggcgc accaccctgc cgcattagga aagactacaa 60
98 cagcactatc gatttattgt gccccacaga ctgttttagg aagcaccag atgtaccta 120
99 tcttaagtgt ggagcgggc cttgggttaa tccaggtgc ctggtta 166
102 <210> SEQ ID NO: 8
103 <211> LENGTH: 166
104 <212> TYPE: DNA
105 <213> ORGANISM: Hepatitis C Virus
107 <400> SEQUENCE: 8
108 tgggactggg ttcaactaaga catgcggcgc accaccctgc cgcattagga gggactgcaa 60
109 cggaaacctc gacctattgt gccccacaga ctgtttcaga aagcaccag atactaccta 120
110 ccttaagtgt ggagcgggc cttgggtgac ccccaaatgc atggtta 166
113 <210> SEQ ID NO: 9
114 <211> LENGTH: 160
115 <212> TYPE: DNA
116 <213> ORGANISM: Hepatitis C Virus
118 <400> SEQUENCE: 9
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120 caacaccttg cgtgccccca ctgattgttt ccgcaagcat ccggaagcca cgtactctcg 120
121 gtgcggctcc ggtccctgga ttacgcccag gtgcctggtc 160
124 <210> SEQ ID NO: 10
125 <211> LENGTH: 160
126 <212> TYPE: DNA
127 <213> ORGANISM: Hepatitis C Virus
129 <400> SEQUENCE: 10
130 tggcacaggg ttaccaaaga cgtgtgggc cccccatgt aacatcggg gggcgggcaa 60
131 taacaccttg acctgcccc cggactgttt ccggaagcac cccgaggcca cttacaccaa 120
132 atgtggttcg gggccttggc tgacacctag gtgcatagtt 160
135 <210> SEQ ID NO: 11
136 <211> LENGTH: 164

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RAW SEQUENCE LISTING DATE: 12/18/2000
 PATENT APPLICATION: US/09/728,720 TIME: 14:02:22

Input Set : A:\Stanfor1.app
 Output Set: N:\CRF3\12182000\I728720.raw

137 <212> TYPE: DNA
 138 <213> ORGANISM: Hepatitis C Virus
 140 <400> SEQUENCE: 11
 141 ctccactgtt tcacaaaac ttgcggcgca ccaccctgcc gcatcagagc tgactttaat 60
 142 gccagcaacg acctgctgtg cccacggac tgtttcagga agcactctga agccacttac 120
 143 atcaaatgtg gctctggggc cctgtgacgc caaagtgcct gata 164
 146 <210> SEQ ID NO: 12
 147 <211> LENGTH: 167
 148 <212> TYPE: DNA
 149 <213> ORGANISM: Artificial Sequence
 151 <220> FEATURE:
 152 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 154 <400> SEQUENCE: 12
 155 tgggactygg ttcactaaga catgcggtgc accaccttgc cgcattagga gggactgcaa 60
 156 cggaaacctc gacctattgt gcccacaga ctgtttcaga aagcaccag atactaccta 120
 157 ccttaagtgt ggagcggggg ccttggttga ccccaaatg catggtta 167
 160 <210> SEQ ID NO: 13
 161 <211> LENGTH: 8
 162 <212> TYPE: PRT
 163 <213> ORGANISM: Artificial Sequence
 165 <220> FEATURE:
 166 <223> OTHER INFORMATION: Description of Artificial Sequence: Flag Epitope
 168 <400> SEQUENCE: 13
 169 Asp Tyr Lys Asp Asp Asp Asp Lys
 170 1 5
 173 <210> SEQ ID NO: 14
 174 <211> LENGTH: 10
 175 <212> TYPE: PRT
 176 <213> ORGANISM: T7 Bacteriophage
 178 <400> SEQUENCE: 14
 179 Met Ala Ser Met Thr Gly Gly Gln Met Gly
 180 1 5 10
 183 <210> SEQ ID NO: 15
 184 <211> LENGTH: 15
 185 <212> TYPE: PRT
 186 <213> ORGANISM: Artificial Sequence
 188 <220> FEATURE:
 189 <223> OTHER INFORMATION: Description of Artificial Sequence: S-Tag Sequence
 191 <400> SEQUENCE: 15
 192 Lys Glu Thr Ala Ala Lys Phe Glu Arg Gln His Met Asp Ser
 193 1 5 10 15
 196 <210> SEQ ID NO: 16
 197 <211> LENGTH: 20
 198 <212> TYPE: DNA
 199 <213> ORGANISM: Hepatitis C Virus
 201 <400> SEQUENCE: 16
 202 cgcgcacraa gtaggyact 20
 205 <210> SEQ ID NO: 17
 206 <211> LENGTH: 21

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RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/728,720

DATE: 12/18/2000
 TIME: 14:02:22

Input Set : A:\Stanfor1.app
 Output Set: N:\CRF3\12182000\I728720.raw

207 <212> TYPE: DNA
 208 <213> ORGANISM: Hepatitis C Virus
 210 <400> SEQUENCE: 17
 W--> 211 cgcatggcggggaytgat g 21
 214 <210> SEQ ID NO: 18
 215 <211> LENGTH: 32
 216 <212> TYPE: DNA
 217 <213> ORGANISM: Hepatitis C Virus
 219 <400> SEQUENCE: 18
 220 cgaagcttca tatgatcgt ggtgctcact gg 32
 223 <210> SEQ ID NO: 19
 224 <211> LENGTH: 38
 225 <212> TYPE: DNA
 226 <213> ORGANISM: Hepatitis C Virus
 228 <400> SEQUENCE: 19
 229 gcggatccct gcagctacaa actggcttga agaatcca 38
 232 <210> SEQ ID NO: 20
 233 <211> LENGTH: 34
 234 <212> TYPE: DNA
 235 <213> ORGANISM: Hepatitis C Virus
 237 <400> SEQUENCE: 20
 238 cgcatatgga gctcgcgggg gcccaactggg gagt 34
 241 <210> SEQ ID NO: 21
 242 <211> LENGTH: 38
 243 <212> TYPE: DNA
 244 <213> ORGANISM: Hepatitis C Virus
 246 <400> SEQUENCE: 21
 247 gctctagact gcagctatat gccagcctgg agcaccat 38
 250 <210> SEQ ID NO: 22
 251 <211> LENGTH: 34
 252 <212> TYPE: DNA
 253 <213> ORGANISM: Hepatitis C Virus
 255 <400> SEQUENCE: 22
 256 cgcctgagcc atggttggcg gggctcattg gggc 34
 259 <210> SEQ ID NO: 23
 260 <211> LENGTH: 40
 261 <212> TYPE: DNA
 262 <213> ORGANISM: Hepatitis C Virus
 264 <400> SEQUENCE: 23
 265 tcgaattcgg atcctacaaa gcacctttta ggagataagc 40
 268 <210> SEQ ID NO: 24
 269 <211> LENGTH: 34
 270 <212> TYPE: DNA
 271 <213> ORGANISM: Hepatitis C Virus
 273 <400> SEQUENCE: 24
 274 cgcctgagcc atggttttcg gcggccattg ggtg 34
 277 <210> SEQ ID NO: 25
 278 <211> LENGTH: 40
 279 <212> TYPE: DNA

see item 10 on Ena Summary sheet

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RAW SEQUENCE LISTING

DATE: 12/18/2000

PATENT APPLICATION: US/09/728,720

TIME: 14:02:22

Input Set : A:\Stanfor1.app

Output Set: N:\CRF3\12182000\I728720.raw

280 <213> ORGANISM: Hepatitis C Virus
 282 <400> SEQUENCE: 25
 283 tcgaattcgg atcctacaga gacgctttaa ggaggttaggc 40
 286 <210> SEQ ID NO: 26
 287 <211> LENGTH: 23
 288 <212> TYPE: DNA
 289 <213> ORGANISM: Hepatitis C Virus
 291 <400> SEQUENCE: 26
 W--> 292 tgggttcggbt gywcnaggat gaa 23
 295 <210> SEQ ID NO: 27
 296 <211> LENGTH: 26
 297 <212> TYPE: DNA
 298 <213> ORGANISM: Hepatitis C Virus
 300 <400> SEQUENCE: 27
 W--> 301 taatgccana rckrtanng gtagtc 26
 304 <210> SEQ ID NO: 28
 305 <211> LENGTH: 379
 306 <212> TYPE: PRT
 307 <213> ORGANISM: Artificial Sequence
 309 <220> FEATURE:
 310 <223> OTHER INFORMATION: Description of Artificial Sequence: Pdisplay Vector
 311 Sequence with E2 insert of Sflb-E2
 313 <400> SEQUENCE: 28
 314 Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
 315 1 5 10 15
 317 Gly Ser Thr Gly Asp Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Gly Ala
 318 20 25 30
 320 Gln Pro Ala Arg Ser Thr Thr Tyr Thr Gly Gly Ala Ala Ser Arg
 321 35 40 45
 323 Thr Thr Gly Thr Phe Thr Ser Leu Phe Asn Ala Gly Ser Ser Gln Lys
 324 50 55 60
 326 Ile Gln Leu Ile Asn Thr Asn Gly Ser Trp His Ile Asn Arg Thr Ala
 327 65 70 75 80
 329 Leu Asn Cys Asn Asp Ser Leu Asn Thr Gly Phe Leu Ala Ala Leu Phe
 330 85 90 95
 332 Tyr Val His Arg Phe Asn Ala Ser Gly Cys Pro Ala Arg Met Ala Ser
 333 100 105 110
 335 Cys Arg Ser Ile Asp Ala Phe Asp Gln Gly Trp Gly Pro Ile Thr Tyr
 336 115 120 125
 338 Ala Glu Ser His Ser Ser Asp Gln Arg Pro Tyr Cys Trp His Tyr Ala
 339 130 135 140
 341 Pro Lys Pro Cys Gly Ile Val Pro Ala Ser Gln Val Cys Gly Pro Val
 342 145 150 155 160
 344 Tyr Cys Phe Thr Pro Ser Pro Val Val Val Gly Thr Thr Asp His His
 345 165 170 175
 347 Gly Val Pro Thr Tyr Ser Trp Gly Glu Asn Glu Thr Asp Val Leu Leu
 348 180 185 190
 350 Leu Asn Asn Thr Arg Pro Pro Gln Gly Asn Trp Phe Gly Cys Thr Trp
 351 195 200 205

*see item 10
on Enr Summary Sheet*

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VERIFICATION SUMMARY

DATE: 12/18/2000

PATENT APPLICATION: US/09/728,720

TIME: 14:02:23

Input Set : A:\Stanfor1.app

Output Set: N:\CRF3\12182000\I728720.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application Number
L:211 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:17
L:211 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:17
L:211 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:17
L:211 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:17
L:211 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:17
L:292 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:26
L:292 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:26
L:292 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:26
L:292 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:26
L:292 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:26
L:301 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:27
L:301 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:27
L:301 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:27
L:301 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:27
L:301 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:27

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